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ALIGNMENTS

Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss. Rice sucrose synthase 3 promoter obtainable from plant genus Oryza, useful for expressing nucleotide sequence of interest in specific tissue or cell type e.g. endosperm. Nucleotide sequence of a rice sucrose synthase 3 (RSus3) promoter. Claim 1; Page 142; 144pp; English. BP. 15-JUN-2000; 2000WO-GB002641. AAF24785 standard; DNA; 1772 99GB-00014210. Donaldson IA, Rasmussen TB; (first entry) WPI; 2001-071398/08. (DANI-) DANISCO AS. WO200078975-A2. Oryza sativa. 17-JUN-1999; 28-DEC-2000. 20-APR-2001 AAF24785; RESULT 1 AAF24785

The present sequence represents a rice sucrose synthase 3 (RSus3) promoter. The RSus3 promoter has low homology with the RSus1 and RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably, the promoter is used to cause expression of a nucleotide of interest the promoter is used to cause expression of a sucrose metabolism, in a plant can affect carbohydrate metabolism, such as sucrose metabolism, in a plant

Sequence 1772 BP; 540 A; 368 C; 374 G; 490 T; 0 U; 0 Other;

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Rice; sucrose synthase 3 promoter; RSus3 promoter; endosperm expression; transgenic plant; carbohydrate metabolism; sucrose metabolism; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice sucrose synthase 3 promoter obtainable from plant genus Oryza, useful for expressing nucleotide sequence of interest in specific tissue
                                                                                                                                                                                                                                                                                                                            expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a rice sucrose synthase 3 (RSus3) promoter. The RSus3 promoter has low homology with the RSus1 and RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transpent plant. Preferably, the promoter is used to cause expression of a mucleotide of interest that caffect carbohydrate metabolism, such as sucrose metabolism, in a plant
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transgenic plant; carbohydrate metabolism; sucrose metabolism;
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obtainable from plant genus Oryza, sequence of interest in specific tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a rice sucrose synthase 3 (RSus3) promoter fragment. The RSus3 promoter has low homology with the RSus1 a RSus2 promoters (7.7% and 4.6%, respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably, the
                                                                                                                                        GCTGAAGCTTTTACGATCCCCATACCGCCGTTGCTAAAACCTGCCAAGAAAAAACA
                                                                                                                                                                                                                                                                                               GAAACAGGTGTCATTTTGTGGTGGAAAGCCAAGTAAAGTAAACAGAAGATGGAAGATAGT
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                                                              AGCTGTCCTGGGAAGGACGGTTTTGGTTGGGATTGTGAACCCTGGTTACTGCACTTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a sucrose synthase 3 (RSus3) promoter fragment.
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 GCATGCATGGCTCTTGTGAAAACAAAAAGGTTACTGGTAAATGACATGCTGCTGTAGCT
                        AGTTAGCAGAATGCAAGGCCCATGCATATGCAATGCTATGCAACAAGTATAGTACCAGCA
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an unifiected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 2000 BP; 520 A; 394 C; 427 G; 658 T; 0 U; 1 Other;

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response of a plant of ing plant

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Hou Y; I, Zou

SA, Ho Zhu T,

J, Goff Xie Z,

Glazebrook Whitham S,

Х,

Cooper 3, Tao

Chang H, Chen W, Co Katagiri F, Quan S, WPI; 2003-175290/17.

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(SYGN) SYNGENTA PARTICIPATIONS

22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105 Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting

Claim 27; SEQ ID NO 6505; 899pp; English.

gene expression

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Score 660; DB 7; L. Pred. No. 3.8e-301; 0; Mismatches 5;
 Query Match 37.2%;
Best Local Similarity 99.4%;
Matches 1090; Conservative
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, bacterial infection; fungal infection; viral infection; rice; ds.

Rice gene, SEQ ID 6505

Plant; gene;

20-NOV-2003

ADA73179

WO2003000898-A1 Oryza sativa

03-JAN-2003

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ADA73179 standard; DNA; 2000

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obtainable from plant genus Oryza, sequence of interest in specific tissue

Disclosure; Page 143; 144pp; English.

Rice sucrose synthase 3 promoter useful for expressing nucleotide or cell type e.g. endosperm.

WPI; 2001-071398/08.

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The present sequence represents a rice sucrose synthase 3 (RSus3) promoter fragment. The RSus3 promoter has low homology with the RSus1 and RSus2 promoters (7.7% and 4.6% respectively). In addition, apart from conserved TATA box and intron splice sites, they have no motifs in common. The promoter can be used to prepare a product of interest, especially in the endosperm of a transgenic plant. Preferably, the promoter is used to cause expression of a nucleotide of interest that can affect carbohydrate metabolism, such as sucrose metabolism, in a plant
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                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 5e-30;
ive 0; Mismatches 0; Indels
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Zhu
                                                                                                                                                                                   Sequence 86 BP; 13 A; 29 C; 16 G; 28 T; 0 U; 0 Other;
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Whitham S, Xie Z,
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Les 86; Conservative
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Plant; bacterial infection; fungal infection; viral infection; rice;

Rice gene, SEQ ID 5846

20-NOV-2003

ADA72521

Zon G;

Hou Y;

Goff SA, Ho e Z, Zhu T,

Xie Z,

Glazebrook J, Whitham S, X

Cooper B, S, Tao Y,

Chen W, Co

Œ,

Chang H,

(SYGN) SYNGENTA PARTICIPATIONS AG.

22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105

WO2003000898-A1

03-JAN-2003

Oryza sativa.

gene; ds.

ADA72521 standard; DNA; 2000 BP.

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T, Zou G;
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                   Sequence 2000 BP; 623 A; 475 C; 360 G; 539 T; 0 U; 3 Other;
                                                                                 Length 2000;
                                                                                                                                                                                                                                                                      294 CAAATTTTTTAATAAGACGAGTGGTCAAACAGTACAAGTAAAAA 250
                                                                                                                                                                                                        90
                                                                                                                                           0; Indels
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Whitham S, Xie Z,
                                                                          DB 7; Le
1.1e-10;
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100.0%; Pred. No. 1.7
:ive 0; Mismatches
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                                                                          2.5%; Score 45;
100.0%; Pred. No.
:ive 0; Mismatc
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Matches 34; Conservative
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                                                                                                              Local Similarity
les 45; Conserv
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Katagiri F,
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                             t 6
                                                                                                                                                                                                                                                                                                                                                          Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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Matches 32; Conservative
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance to a plant to bacterial, fungal or viral infection. The present sequence was used to
  Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice; lesion formation inhibition; heat stress; agriculture; Spl7; transgenic; plant; horticulture; gene; ss.
                                                                                                                                                                                                                                                                                     Query Match 1.6%; Score 28; DB 7; Length 2000; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          Sequence 2000 BP; 638 A; 344 C; 433 G; 583 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice lesion inhibitor protein Sp17 coding sequence
                                                                                                                                                                                                                                                                                                                                                               292 AAAATAATAATAATTCCAAATTTTTT 319
                                                                      Claim 27; SEQ ID NO 6668; 899pp; English
                                                                                                                                                                                                                                                                                                                                              29 AAAATAAATAATACCAAATTTTTT 56
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/product= "Sp17"
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3711. .5327
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illustrate the invention.
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P-PSDB; AA017798.
                                               gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                              Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                            Zou G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2000 BP; 613 A; 404 C; 328 G; 655 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 2000;
0.0013;
hes 0; Indels
                                                                                                                        Goff SA, Hor
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Whitham S, Xie Z, Zhu T,
                                                                                                                             Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 AAATTTTTTTAATAAGACGAGTGGTCAAAC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%; Score 30; DB 100.0%; Pred. No. 0.Ctive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 AAATTTTTTTAATAAGACGAGTGGTCAAAC 76
                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 6531; 899pp; English.
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                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA73342 standard; DNA; 2000 BP
                                                                                                                           Cooper B, S, Tao Y,
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S, Tao Y,
                                         22-JUN-2001; 2001WO-IB001105
                                                                   22-JUN-2001; 2001WO-IB001105
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                                                                                                                                       Ouan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang H, Chen W, Co
Katagiri F, Quan S,
                                                                                                                                                                     WPI; 2003-175290/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-175290/17
                                                                                                                           Chen W,
                                                                                                                                                                                                                                         gene expression.
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                                                                                                                          Chang H, Che
Katagiri F,
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             03-JAN-2003
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Matches
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Gaps

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Length 2000;

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Rice-originated gene, Sp17, that inhibits lesion formation and is applicable in improving heat stress of plants thus leading to prevention of lesion formation, for developing new breeds of plants for agriculture and horticulture.
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Claim 1; Page 30-40; 53pp; Japanese.

The present invention provides the protein and coding sequences of rice lesion formation inhibitor Sp17. The protein improves the heat stress of the plant, and can be used in the development of new breeds of plants for agriculture and horticulture. The present sequence is the coding sequence the invention

Sequence 5579 BP; 1453 A; 1272 C; 1235 G; 1619 T; 0 U; 0 Other;

Gaps ; 0 Query Match
1.6%; Score 28; DB 6; Length 5579;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 57 AATAAGACGAGTGGTCAAACAGTACAAG 84 ð

;

2210 AATAAGACGAGTGGTCAAACAGTACAAG 2183

g

ADA73166/

ADA73166 standard; DNA; 2000 BP

ADA73166;

(first entry) 20-NOV-2003

SEQ ID 6492 Rice gene,

Plant; bacterial infection; fungal infection; viral infection; rice; d8 gene;

Oryza sativa.

WO2003000898-A1.

03-JAN-2003

22-JUN-2001; 2001WO-IB001105

22-JUN-2001; 2001WO-IB001105

(SYGN) SYNGENTA PARTICIPATIONS AG

Hou Y; F, Zou G; J, Goff 8 Xie Z, 2 Glazebrook Whitham S, Α, Cooper I Chen W, Co Œ, Chang H, Katagiri

The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, thugal or viral infection. The present sequence was used to

t 6

Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant

Claim 27; SEQ ID NO 6524; 899pp; English.

gene expression.

WPI; 2003-175290/17.

22 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression

Claim 27; SEQ ID NO 6492; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

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Gaps

.; 0

1.5%; Score 26; DB 7; Length 2000; 100.0%; Pred. No. 0.1; tive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 26; Conservative

Query Match

AAF81474 standard; DNA; 676 BP

RESULT 15 AAF81474/ ID AAF8: XX

Sequence 2000 BP; 633 A; 407 C; 355 G; 604 T; 0 U; 1 Other;

illustrate the invention.

Sequence 2000 BP; 492 A; 534 C; 468 G; 504 T; 0 U; 2 Other;

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                  Gaps
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e Z, Zhu T,
                  Indels
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Whitham S, Xie Z,
                 0
   DB 7;
0.1;
1.5%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                                             1060 ACTTTAGATAATAAAGTAAGTCACAA 1035
                                 1 ACTITAGATAATAAAGTAAGTCACAA 26
                                                                                                                                                                                                                                         (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                    ADA73198 standard; DNA; 2000 BP.
                                                                                                                                                                                                                                                        Cooper B, S, Tao Y,
                                                                                                                                                                                                              22-JUN-2001; 2001WO-IB001105.
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                                                                                                                 (first entry)
                   26; Conservative
                                                                                                                              Rice gene, SEQ ID 6524
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          Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                 WO2003000898-A1.
                                                                                                                                                                  Oryza sativa.
                                                                                                                 20-NOV-2003
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                                                                                                   ADA73198;
      Query Match
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                                                                     RESULT 14
ADA73198
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The present invention relates to novel corn promoter sequences (see AAF81456-AAF81478). The promoter sequences are useful for conferring expression of a second polymucleotide molecule in a transgenic plant tissue. In addition, the promoter sequences are useful for providing plants with herbicide resistance. The promoter sequences are suitable for selectively modulating expression of any operatively linked gene and provide additional regulatory element diversity in a plant expression vector in gene stacking approaches. The present sequence is one such corn promoter sequence isolated in the present invention
                                                                                                                                                                                                                                                                                                                                                                                Novel promoter nucleic acid sequences useful for regulating heterologous gene expression in plants, comprising regulatory sequences located upstream to plant DNA structural coding sequences.
                                                                                             Corn; promoter; transgenic plant; herbicide resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 98; 101pp; English.
                                                                                                                                                                                                                                                                                                                      Chen G,
                                                          Corn promoter clone #700345819.
                                                                                                                                                                                                                       13-SEP-2000; 2000WO-US025078.
                                                                                                                                                                                                                                                      99US-0154182P
                              (first entry)
                                                                                                                                                                                                                                                                                                                   Anderson HM, Chay CA,
                                                                                                                                                                                                                                                                                    (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-244796/25.
                                                                                                                                                         WO200119976-A2
                                                                                                                                                                                                                                                      16-SEP-1999;
                            08-JUN-2001
                                                                                                                                                                                         22-MAR-2001
                                                                                                                           Zea mays.
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Conner TW;

0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 24; Conservative 0; Mismatches 0; Indels Sequence 676 BP; 210 A; 152 C; 119 G; 195 T; 0 U; 0 Other;

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51 TITITAATAAGACGAGTGGTCAA 74

g à

Search completed: October 2, 2004, 10:13:35 Job time : 1029 secs

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RESULT 2
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US-09-7594-3/C
; Sequence 3, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; FILE REPERENCE: CLO101043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
LINNICTH. 90541
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Matches 24; Conserv
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US-09-665-189A-71
TYPE: DNA
ORGANISM: Human
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TYPE: DNA
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Sequence 3, Appli
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Sequence 6, Appli
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Sequence 3, Appli
Sequence 37, Appl
                                                            October 2, 2004, 08:40:19 ; Search time 153 Seconds (without alignments) 6427.274 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-497-855A-37

US-09-413-294A-292

US-09-113-294A-292

US-09-113-204C-13

US-08-464-517-30

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US-08-463-772-30

US-08-642-274D-39

US-08-642-274D-39

US-09-134-001C-301

US-09-134-001C-301

US-09-27-357-31

US-09-227-357-31

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US-09-621-976-15602
PCT-US92-03993-6
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US-09-326-480A-4
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                                                                                                                                                                         682709 segs, 277475446 residues
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                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                       Gapop_60.0 , Gapext 60.0
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GENERAL INFORMATION:
APPLICANT: Chay, Catherine
APPLICANT: Chay, Catherine
APPLICANT: Chen, Guilan
APPLICANT: Chen, Guilan
APPLICANT: Conner, Timothy
TITLE OF INVENTION: Plant Regulatory Sequences for Control of Gene Expression
TITLE OF INVENTION: 18-211(15674)B
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/665,189
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
SEQ ID NOS: 75
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
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US-09-322-478-35
US-09-342-681C-5
US-09-134-000C-1679
US-09-543-681A-1750
US-09-543-681A-1750
US-09-976-594-764
US-09-976-594-764
US-09-976-594-764
US-09-977-419C-3
US-09-177-419C-3
US-09-177-419C-3
US-09-177-419C-3
US-09-137-419C-3
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US-09-322-478-21
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US-09-9253-682-1
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US-09-9253-682-1
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US-09-9253-682-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 rrrrraaradacdagregreaa 203
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; Sequence 71, Application US/09665189A
; Patent No. 6645765
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TYPE: DNA ORGANISM: Zea mays FEATURE:
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NAME/KEY: unsure
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                                                                                                                                                                                                                                                           Sequence 37, Application US/09497855A

Patent NO. 6655432

GENERAL INFORMATION:

APPLICANT: Huang, Tim

TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION

FILE REFERENCE: UOO12-03

CURRENT APPLICATION NUMBER: US/09/497,855A

CURRENT FILING DATE: 2000-02-04

PRIOR PRILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-05

NUMBER OF SEQ ID NOS: 54

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SEQ ID NOS: 54
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: UNO1523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT PILING DATE: 1099-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
STOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
SOFTWARE: PLACATION NUMBER: 60/118,760
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 44
LENGTH: 193303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                               Gaps
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1.3%; Score 23; DB 4; Length 193303;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 23; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 23; DB 4; Length 193303;
100.0%; Pred. No. 0.32;
tive 0; Mismatches 0; Indels 0;
                                  1.3%; Score 23; DB 4; Length 90541;
100.0%; Pred. No. 0.33;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166834 AGTITICOTOCIONICACIONAS 166856
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                                                                                                                                                      17920 AAGTAAGTCACAAGAAAATAAA 17898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1744 AGTITCCTCCTCTTCTCTTCAG 1766
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                                                                                                                        14 AAGTAAGTCACAAGAAAAAAAA 36
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18-09-447-855A-44
'Sequence 44, Application US/09497855A,
'Patent No. 6605432
                                                                               23; Conservative
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Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens;
US-09-497-855A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens;
US-09-497-855A-44
                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 193303
                                                                                                                                                                                                                           RESULT 3
US-09-497-855A-37
JS-09-759-359A-3
                                        Query Match
                                                                             Matches
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Sequence 13, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynn Doucetee-Stamm et al

APPLICANT: Lynn Doucetee-Stamm et al

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/065,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-10-08

NUMBER OF SEQ ID NOS: S674

SEQ ID NO 13

LENGTH: 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (505)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-134-001C-13
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Sequence 29. Application US/09313294A

Sequence 29. Application US/09313294A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN BAR FILE REFERENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 292
ILBRIGHT: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
OTHER INFORMATĪON: Incyte ID No. 6476212 700548929H1
NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.1%; Score 20; DB 4;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 20; DB 100.0%; Pred. No. 9.9 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 2, 6, 75-93
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1285 GTTGGTAAACCAGCAAAAT 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 950 AGCAGCAGCATGCATG 969
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Best Local Similarity 100.
Matches 20; Conservative
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Sequence 30, Application US/08463772
Patent No. 606501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: join(378..569, 662..1000, 1040..1189, ; LOCATION: 1191..1292, 1292..1324)
US-08-246-361A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 20; DB 2;
100.0%; Pred. No. 9.7;
cive 0; Mismatches
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 AAAAACAAAACAAACACAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 AAAAACAAAACAAACACAC
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Best Local Similarity 100.0
Matches 20; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΜA
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                                          NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
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Sequence 30, Application US/08246361A
Sequence 30, Application US/08246361A
Sequence 30, Application US/08246361A
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1462; 9.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.1%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 9.7
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMUTUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIPICATION: 435
FICH SAPPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1992
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AAAAACAAAAACAAACACAC 177
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                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1462 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                          USA
                                                                                                                                                                                                       02109
                                                                                                                                                                      STATE: MA
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LOCATION:
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                                                                                                                                                                                        COUNTRY:
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Gaps

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Indels

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GENERAL INCRMATION:
APPLICANT: SHIGH, YOSEF
APPLICANT: SHIGH, YOSEF
APPLICANT: SHIGH, YOSEF
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 220
SOCTHWARE: PATENTIN Ver. 2.1
SEQ ID NO 39
LENGTH: 531
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; OTHER INFORMATION: Description of Artificial Sequence: genomic
US-08-642-274D-39
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                                                                                                                                   Indels
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APPLICATION NUMBER: US/08/952,014C
FILING DATE:
                                                                                       Query Match
1.1%; Score 20; DB 5;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.1%; Score 19; DB 3; Best Local Similarity 100.0%; Pred. No. 30; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290.00028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           US-08-642-274D-39; Sequence 39, Application US/08642274D: Patent No. 6200749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1321 AATTTTAAATTTTAGTTTT 1339
                                                                                                                                                                                                                          310 AAAAACAAAACAAACACAC 329
                                                                                                                                                                                 158 AAAAACAAAACAAACACAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 AATTTTAAATTTTAGTTTT 123
                       MOLECULE TYPE: DNA (genomic) PCT-US93-05000-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-952-014C-39
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TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.1%; Score 20; DB 3; Length 1462; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 20; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: PCT/US93/05000

FILING DATE: 19930525

CLASSIFICATION DATA:

APPLICATION NUMBER: US/07/888,178

FILING DATE: 26-M8-1992

ATTORNEY/ACENT INFORMATION:

NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
STREET: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(378..569, 662..1000, 1040..1189, 1191..1292, 1292..1324)
                                                                                                                                                     NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REBENCE/DOCKET NUMBER: MII-004C
TELECOMUTUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
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                    APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application PC/TUS9305000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 AAAAACAAAAACAAACACAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 AAAAACAAAACAAACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: CSF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 300: SEQUENCE CHARACTERISTICS:
LENGTH: 1462 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
    16-OCT-1992
                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US93-05000-30
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                               Length 851;
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; OTHER INFORMATION: Incyte ID No. 6492505 1516908CB1
US-09-495-050A-138
                                                                                    4.
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZ010P1
                                                                            Query Match 1.1%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 29; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER FILING DATE: 1999-01-08
EARLIER FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,931
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APPLICATION NUMBER: 60/051,928
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EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/056,360
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Patent No. 6342581
GENERAL INFORMATION:
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US-09-227-357-31/c
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US-09-495-050A-138/C
Sequence 138, Application US/09495050A
Sequence 138, Application US/09495050A
Sequence 138, Application US/09495050A
Sequence 138, Application US/09495050A
GENERAL INFORMATION:
APPLICANT: Guegler, Karl, J.
APPLICANT: AL-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED FILE REFERENCE: PA-0013 US
CURRENT FILING DATE: PA-0013 US
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PREL PROGRAM
SEQ ID NO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1996-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 301
LENGTH: 573
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30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                         1321 AATTTTAAATTTTAGTTTT 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AATTTTAAATTTTAGTTTT 123
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              TELEFAX: 810-539-5055
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 TAAATCATTTTTAGTTGCT 81
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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US-09-134-001C-301/c
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Query Match
1.1%; Score 19; DB 4; Length 2095;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER PELICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-09-12

SOFTWARE: PATON NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12

SOFTWARE: PATON NUMBER: 1997-09-12

SOFTWARE: PATON NUMBER: 1997-09-12

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Search completed: October 2, 2004, 15:15:58 Job time: 157 secs

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Sequence 87728, A
Sequence 64432, A
Sequence 86792, A
Sequence 43365, A
Sequence 13365, A
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Sequence 2163, Ap
Sequence 10006, A
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Sequence 92628, A
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Sequence 27816, A
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7511.097 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/DSO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUB_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-437-963-92628
US-10-168-273B-1
US-10-260-238-1731
US-10-425-114-718
US-10-425-114-718
US-10-260-238-2163
US-10-437-963-10006
US-10-260-238-1731
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 4401, Ap Sequence 59741, A	91213,	36681,		1, Apr	258,	45,		409,		1826,	Н	ě	e.	m	Sequence 37, Appl	4	a)	g	12335,			Sequence 216612,	1722,	1963,	2448,		263, 7	385,	
US-10-437-963-4401 US-10-437-963-59741	-10	US-10-437-963-36681	US-10-260-238-1664	US-10-168-273B-1	US-10-240-453-258	US-10-239-676-45	US-10-311-455-619	US-10-221-714A-409	US-10-311-455-118	US-10-311-455-1826	US-10-311-455-1341	US-09-759-359A-3	US-10-20	US-10-799-676-3		₽	US-10-312-841-1	US-10-424-599-91097	US-10-425-114	us-1	US-10-027-632-	US-10-027-632-216612	US-10-260-238-1722	US-10-260-		US-10-424-599-3866	US-10-221-613-263	US-10-311-455-385	US-10-311-455-875
17	13	17	16	13	15	15	15	13	15	15	15	σ	15	17	15			13	13	13	13	16	16	16	16	13	13	15	15
433 981	1220	1256	2000	5579	6533	6544	6544	7442	9052	9267	9817	90541	90541	90541	193303	193303	3673778	222	574	574	1241	1241	1912	2000	2000	3061	6061		7276
1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2	•	1.2	•	1.2	1.2
23 23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	22	22	22	22	22	22	22	22	22	22	22	22
15 16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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APPLICANT: Li, Ping,
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 7688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%; Score 39; DB 17; Length 1610;
100.0%; Pred. No. 7.7e-09;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_1425C.1
US-10-437-963-7688
                    Sequence 7688, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                          Boukharov, Andrey A.
Barbazuk, Brad
                                                                                             APPLICANT: La Roga, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                        GENERAL INFORMATION:
US-10-437-963-7688/c
                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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39 CCAACGCTCACCGATGGGTGCCTCTCGACCACGAGTTTA 1 815 CCAACGCTCACCGATGGGTGCCTCTCGACCACGAGTTTA

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Yibua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT PILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 27816
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GOSE, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Shown NUMBER: US/10/260,238
CURRENT APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PLILNG DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SQUID NOS: 6077
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                                                                        2210 AATAAGACGAGTGGTCAAACAGTACAAG 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1064 AATAAGACGAGTGGTCAAACAGTACAA 1038
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                         57 AATAAGACGAGTGGTCAAACAGTACAAG
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                                                                                                                                                                                                         Sequence 1731, Application US/10260238 Publication No. US20040016025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: Budworth, Paul R. APPLICANT: Moughamer, Todd G. APPLICANT: Briggs, Steven P. APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1731
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ORGANISM: Oryza sativa
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NAME/KEY: unsure
                                                                                                                                                                                US-10-260-238-1731/c
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US-10-437-963-27816
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Sequence 92628, Application US/10437963
; Sequence 92628, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Briansuk, Brad
; APPLICANT: Briansuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants (19792)
; CURRENT APPLICATION NUBBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 92628
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Sequence 1, Application US/10168273B

Sequence 1, Application US/10168273B

Publication No. U220040058324A1

GENERAL INFORNATION:

APPLICANT: Yamo, Masahiro

APPLICANT: Yamo, Masahiro

APPLICANT: Yamo PLANT LESTON FORMATION SUPPRESSING GENE, Spl7 AND USE THEREOF

TITLE OF INVENTION: PLANT LESTON FORMATION SUPPRESSING GENE, Spl7 AND USE THEREOF

FILE REFERENCE: 23572-005 NATL

CURRENT FILING DATE: 2003-03-27

PRIOR PRING DATE: 2001-10-18

PRIOR PLILING DATE: 2000-10-18

PRIOR FILING DATE: 2000-10-18

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 5579
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100.0%; Pred. No. 0.0037;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 37; DB 17; Length 29 ilarity 100.0%; Pred. No. 8.5e-08; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1727 GCTCTGTTCATCCATAGAGTTTCCTCCTCTTCTCCTT 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 GCTCTGTTCATCCATAGAGTTTCCTCCTCTTCTCCTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_91091C.1 US-10-437-963-92628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(2981)
OTHER INFORMATION: unsure at all n locations
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Best Local Similarity 100.
Matches 28; Conservative
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NAME/KEY: CDS
LOCATION: (3711)..(3947)
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; LOCATION: (4185)..(5327)
US-10-168-273B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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nes 37; Conserv
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Matches
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PRIOR APPLICATION NUMBER: US 60/370,620 PRIOR FLING DATE: 2002-04-04 NUMBER OF SEQ ID NOS: 6077 SEQ ID NO 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      25; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                    TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                 Best Local Similarity
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US-10-437-963-10006/c
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US-10-312-841-2
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                          Query Match
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                                                                                                               LENGIH:
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 718
LENGTH: 858
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APPLICANT: Glazebrock, Jane
APPLICANT: Katagiri, Funiyaki
APPLICANT: Katagiri, Funiyaki
APPLICANT: Kreps, Joe
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
                                                                                                                                                       DB 17; Length 630; 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.4%; Score 25; DB 13; Length 858; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                0; Indels
                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_32474C.1
US-10-437-963-27816
LOCATION: (1)..(630)
OTHER INFORMATION: unsure at all n locations
PEATURE:
                                                                                                                                                    Query Match 1.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
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US-10-425-114-718
                                                                                                                                                                                                                                                                                      428 ACTITAGATAATAAAGTAAGTCACAA 453
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CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
                                                                                                                                                                                                                                             1 ACTITAGATAATAAAGTAAGTCACAA 26
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Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Mouphamer, Todd G.
APPLICANT: Eliggs, Steven P.
APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 718, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-425-114-718/c
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
TITLE SE IOI/12/08/W0
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILLING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Pink
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DAIE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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1.4%; Score 25; DB 16; Length 2000; 100.0%; Pred. No. 0.12; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.13;
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OTHER INFORMATION: Clone ID: PAT_MRT4530_16369C.1
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1.4%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 25; Conservative 0; Mismatches
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                                                                                                                      86 AAAAACTCAAAATTCCTTATATTAT 110
                                                                                                                                                        91 CTCAAAATTCCTTATATTATGGGAC 115
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PUDLICATION NO. USZUUGUIZ334341
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT:
APPLICANT: Brabazuk, Brad
APPLICANT:
CURRENT PILING DATE: 2003-05-14
NUMBER: CBC ID NOS: 204966
SEQ ID NO 43365
LENGTH: 1480
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT PILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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US-10-437-963-43365
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_857C.1
US-10-437-963-86792
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OTHER INFORMATION: unsure at all n locations
     0; Mismatches
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                                                      153 AAGAAAAAACAAAACAAACACA 176
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Publication No. US20040123343A1
GENERAL INFORMATION:
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  24; Conservative
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ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Availe, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Fice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
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APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Acvalic David K
APPLICANT: About Yihua
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 64432
LENGTH: 390
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100.0%; Pred. No. 0.2;
tive 0; Mismatches 0; Indels 0;
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US-10-437-963-87728
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US-10-424-599-64432
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100.0%; Pred. No. 0.34;
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 87728, Application US/10437963; Publication No. US20040123343A1
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                                                                                                                                           Conservative
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Best Local Similarity
Matches 25; Conserva
     ; LOCATION: (379615)
US-10-312-841-2
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Query Match 1.3%; Score 23; DB 17; Length 433; Best Local Similarity 100.0%; Pred. No. 1.1; Matches 23; Conservative 0; Mismatches 0; Indels
                                                FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11289C.1
US-10-437-963-4401
                                                                                                                                                                                                                                                                                                                                                                                          Search completed: October 2, 2004, 18:20:05 Job time: 1204 secs
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TYPE: DNA
ORGANISM: Oryza Bativa
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; Sequence 4401, Application US/10437963
; Publication No. US20040123343A1
; Sequence 4401, Application No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4401
; LENGTH: 433
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APPLICANT: GLOUDEL' FUNDAMENTI GOEFF. Stephen A.
APPLICANT: Kataglir', Funiyaki
APPLICANT: Kataglir', Funiyaki
APPLICANT: Kataglir', Funiyaki
APPLICANT: Kataglir', Funiyaki
APPLICANT: Ricke', Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1731
LENGTH: 2000
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                                                                                                                                                                                                                                                                                                        Sequence 1731, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Cooper, Bret
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ORGANISM: Oryza sativa
                     Query Match
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Matches 24; Conserva
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AP005002 C
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AC136956 C
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AC144491
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                                                             SUMMARIES
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(c) 1993 - 2004 Compugen Ltd.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="nucleic acid sequence"
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ALVUANE SALIVA (japonica cultivar-group) genomic DNA, chromosome 7, BAC clone:B1056G08.
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Oryza sativa (japonica cultivar-group)
Bukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                   /organism="synthetic construct"
/mol_type="unassigned DNA"
/bxref="taxon:32630"
/note="promoter sequence"
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100.0%; Pred. No. 0;
live 0; Mismatches
   Donaldson,I.A. and Rasmussen,T.B. Rice sucrose synthase promoter Patent: WO 0078975-A 6 28-DEC-2000; DANISCO A/S (DK)
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COMMENT

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join(11555. .1934,12176. .12278,12484. .14337,14423. .14478, 14801. .15101)
/gene="B1056G08.106-1"
join(-11555. .11934,12176. .12278,12484. .14246,14423. .14478, 1601. .>15101)
/gene="B1056G08.106-1"
/note="supported by full-length cDNA(s): AK073803"
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14801. .>15636)
/gene="B1056G08.106-2"
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23693. .23845,24429. .26511,26756. .28073,28346. .28429,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(11585. .11934,12176. .12278,12484. .14337,14423. .14478, 14801. .15636)
join(nesserved by full-length cDNA(s): AK073803"
14801. .15636)
join(en="BE056608.106-2"
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join(11828. 11934,12176. 12278,12484. 14246,14423. 14478,
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/gene="B1056G08.106-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein.id="BAC21479.1"
/db_xref="G1:24061479.1"
/db_xref="G1:24061479.1"
/db_xref="G1:24061479.1"
/dranslation="wDLLSAGGRRASPSPPPPLAAAIBAPPSSSPADRAPPLPRRITAPPPDNWTKVTIGSRAPNNPGHIKLTRQSQQLNDLGATSVTQFINYITCRSSSPSDNT
      NPFAIAEFLLCCNLCGVPLAGRPSFIYIGEKAFCKEECRSRYVVEEALREARBEKRRA
AAAAASPEKKKEAAAARKGGEECREGSIFFICADDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative RNA Polymerase II subunit 14.5 kD"
/protein id="BAC21480.1"
/db_xref="GI:24060023"
/translation="MAMSALKFCGECSNMLYPREDKETHTLLYACNSCEHQEPATDTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (8972. .11317)
/gene="B1056G08.105"
complement (join (<8972. .9052,9394. .9552,11110. .11185,
                                                                                                                                                                                                                predicted by GENSCAN
this category is not included in IRGSP standard"
join(7413. .7422,7688. .8096)
/gene="B1056G08.103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          point are not identified" .9052,9394. .9552,11110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="start and end point are not identified"
join(8222. .8568,8759. .8962)
join(8222. .85608.104"
/note="predicted by GeneMark.hmm etc."
                                                                  complement (join (5482. .5716,6013. .6023))
                                                                                                                       complement(join(5482. .5716,6013. .6023))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(<8222. .8368,8759. .>8962)
/gene="B1056G08.104"
                                                                                                                                                                                                                                                                                                                                        join(7413. .7432,7688. .8096)
/gene="B1056G08.103"
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21538. ,28635
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/gene="B1056G08.105"
/note="start and end point
complement(join(8972. .9052
                                                                                                                                                                                      'note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                   'note="hypothetical ORF
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/join(<8222. .8342 parts
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                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted by GENSCAN
                                                                                                                                                          'gene="B1056G08.102"
                                                                                                 /gene="B1056G08.102"
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(Branil: teasakiamias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-741, Fax:81-298-38-7468)

On Oct 16, 2002 this sequence version replaced gi: 22212589.

Genes were predicted from the integrated results of the following: Genses were predicted from the integrated results of the following: Genses were predicted from the integrated results of the following: (http://www.igit.oio/gy/gatech.edu/GeneMark.huml), FGENESH

(http://www.igit.org/tdb/glimmerm/), SplicePredictor

(http://www.igit.org/tdb/glimmerm/), SplicePredictor

(http://www.iigir.org/db/glimmerm/), SplicePredictor

(http://www.iigir.org/software/glimmerm/), BlaASTW and BLASTW. The genomic sequence was searched against NCBI NonRedundant Protein database (http://robi.nlm.nih.gov/blast/db) and the cDNA genomic sequence was searched against NCBI NonRedundant Protein database with BLASTW. ESTS represent the identified cDNA sequences using BLASTW with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequence using minkly with the corresponding DDBJ accession no.

A gene with based on the protein name to indicate the homology to any protein but with full-length cDNAs represent the identificant homology to any protein but with full-length based on the protein name to indicate the homology covering almost the entire length of partial significant homology covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by a single gene prediction program is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from Misrev to -21Mi3 of the BAC clone has an apartial sequence of B1056008 clone. This as partial sequence of B1056008 clone has an overlap with P056008 clone. The sequence o
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RPVPAAAAAAMDDVVGRVARPARPSARAIMEGTHKQISSGGASGGSYCTVPWCSICTGN
                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (27-MAR-2002) Takuji Sasaki, National Institute of
                         Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:B1056G08
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="7"
/clone="B1056G08"
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Gpene="B1055G08.101"

complement (join(3083. .3490,3648. .4070))

/gene="B1056G08.101"
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/gane="B1056G08.101"
/note="contains Set's): AU069911(E12068)
contains full-length cDNA(8): AX108210"
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/protein_id="BAC21478.1"
/db_xref="GI:24060021"
                                                                                                                    Published Only in Database (2002)
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                                                                                                    CTGCGAAATCCGCAGATTGGTTTGTTCAATTCCAACTTGCAGTCCTTCAGATTGGTTGCA
                                                                                                                                         TG'IT-CAACCGTAGTACATCTGAAAATGAAGTGTTAAATACCTTGAGAAGACCTTCATG
                                                                                                                                                                              67924 IGITCCAACCGTAGTACATCTGAAAATGAAGTGTTAAATACCTTGAGAAGACCTTCATG
                                                                                                                                                                                                                       ATTITIGGAGTIAGATTITIAGGGTGTTTCCATCGTAGTGTATTITCTACTATTGCCAGTTTA
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                                                               CTGCGAAATCCGCAGATTGGTTTGTTCAATTCCAACTTGCAGTCCTTCAGATTGGTTGCA
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GARPHDSVSRELVLFADHFGARRLSSCAKRMENSLCQRREDICFPHYSUSSTSGWKSFDD
GANFGSSSSDWSLDFTQADQÇASSINKS I IGGSVSHIFIRSNSQNSVDVPPEPSAVQHPK
PTI QQSVEKQEKETDALPAPAPAGGGSRRLSVQDRINNFESKQKEQTSSSGNSAACTS
KVPPTKGERRRRVPSGARANDKLVRRWNSDMS.TDLSNNDSSSTARRRETGTPVGTPTS
ANLEYNSKARANDGDAAGLKHAVTSCOKODTSDALPLDSTTADAPSSSSTARNTTSPSPLSA
IASSSPQKQTAPRVEDDMVITSSIESESSFRKEVGASGKGDVRMSGQAVSSVSTRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRVNEVKPPLVLPERIYTKQIVKESITNEFDANELLKMVDTEGYNNNVPQSIISLEES
RGKFYDQYMQKRDAKLKEDMKLQGEQKEATIKAMRDSLERSNAEMRAKFSRSSSVPDS
TYISRCAHKPPPLQSVIKDKDQGIDSFLVEEEMNSDYLSGDGSSRSADSRKHFSNKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNQKKSIAPVHRHSERTVSSGYANRRNLPDNPLAQSVPNFADLRKENTKPSAGLSRAA
PRTQPKSFIRSKSIIEESKNISKDQSRKSQSMRKNLSPGELRDATSMNDVIYNWAPSK
ISNDQVEGVFAYITHTAGSTKSFLRKGNEAHPAVGIAGFAPPMFANTYQNGDDDDFLD
                                                                                                                                                                                                                                                              /translation="MEPDAPLDFALFQLSPRRSRCELVVSGNGRTERIASGSVKPFVA
HLRAAEEQAAAQPPPPAIRLQLDRRAAWFSKGTLERFVRFVSTPEVLEMANTFDAEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                           VKTSPR-PTWPENNVTLSSPPLSQEHVQMTDEET1PIVHEVAVKKEQIVQKDNRGSRLR
SKETIHABADVVGRKDRPSRTTGKISOPTRTRATSURSBANDRANFRSSSVRDBAASTBASTBASTHDV
NLQRKSLARKVEDGENVAAGSEILPQSDCSTHQGTNNSRQSSSAEQELSLHGGRVVAL
ISDGNAVPLEQTKRPTKGSQDRHDELQKKANELEKLFAAQKLTSSRRGKSTDVQVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEEDSPDETKDEEYESIBENLRESDPPADSDSENPGISHEFGNSDDPGSENGDVSFPS
DAPTIGGSKFNAFAGNMHDTPGEVPASWSTRPHLFAYANDNSDGDAFADSPNGSPSPW
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GLNDWVSASTASECDDDMEDGRDLAMGSSDDFRKSRMGYPSAYDGFVDTDVFAEQDQS
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                                           /note="start and end point are not identified"
join(21538. .21596,21679. .21858,21962. .22064,22185. .2
23693. .23845,24429. .26511,26756. .28073,28346. .28429,
                                                                                                                                         /note="contains Set's): C26549(C12568),AU092341(C12568) contains full-length cDNA(s): AK109921" /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67504 GTGGTCAAACAGTACAAGTAAAAACTCCAAAATTCCTTATATTATGGGCTTTATATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGGCATGCATCTTAGGTCGGCACATTGAGAGGTCGGCAGTAGACGAGTTACCCTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATAATAAAGTCACAAGAAAAATAAATAATAATTCCAAATTTTTTAATAAGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="B1056G08.108"
<29193. .>31064
/gene="B1056G08.108"
/more="supported by full-length cDNA(s): AK064501"
29193. .31064
                                                                                                                                                                                                   product = "COPI-interacting protein 7 (CIP7)-like"
protein id="BAC21482.1"
/db_xref="GI:24060025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRSSIPNPPANFRLREDQLTGSSLKAPRSFFSLSTFRSKGGDARLR"
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larity 99.3%; Pred. No. 0;
Conservative 0; Mismatches
        28571. .>28635)
/gene="B1056G08.107"
                                                                                                                             /gene="B1056G08.107"
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	Qy 1329 ATTITAGTITTITITAACTIAGCGGGAAACCTIGAAGTITGTGCTGTGGAGCTGT 1386 bb 661 ATTITAGTITTITITTTTTTAACTIAGCGGGAAACCTTGAAGTTTGTGCTGTCGAGCTGT 720 Qy 1387 CCTGGGAAGGACGGTTTTGGTTGGGAATTGTGAACCTTGTTTTTTGAA 1446 Db 721 CCTGGGAAGGACGGTTTTGGTTGGGAATTGTGAACCTTGGTTTACTGCTTTTTTTT	Db 1021 CAGGTGGATGCTCTCCCAGCATCCATCGGTTCTGCTCTGTTCATCCATC	AX063523 LOCUS AX063523 LOCUS AX063523 AX065352 AX065352 AX065352 AX065352 AX065352 AX065352 AX065352 AX065352 AX063523 AX063523.1 GI:12541262 SURRING SYNTHETIC CONSTRUCT ORGANISM SYNTHETIC CONSTRUCT ATITLE AUTHORS Donaldson, I.A. and Rasmussen, T.B. TITLE AUTHORS DAISCO A/S (DK) DAISCO A/S (DK) FRATURES SOURCE 1.86 BENERAL DAISCO A/S (DK) FRATURES 1.86
Db 68884 GAACAGATATTAGTGCAACAGACAATTTTTTTTTTTTTT	AX656635 AX656635 AX656635 DEFINITION Sequence 6505 from Patent W003000898. ACCESSION AX656635 AX656635 AX656635 AX656635 AX656635 Oryza sativa ORGANISM AX656635 Oryza sativa ORGANISM	5; Indel CATTTATAAN 	QY 729 TCGTTCATTTTCTACCACTTATCAACTGATCAATTGACAATAAAAGTT 788 Db 61 TCGTTCATTTTTCTACCACTTATCAACCATAGCTCAACGATCAATTGACAATAAAAGTT 120 QY 789 ACTAAACGACATCGCTCATCACCACCGATCGATCGACCACCAGA 848 Db 121 ACTAAACGACATCGCTCATCACACCCAACGCTCACCGATCGACCACGA 180 QY 849 GTTTAGCACTTGTCAACAATATATGCGTCACCGATCAACTGATCGACCACGACAGAT 908 Db 181 GTTTAGCACTTGTCAACAATATATGCGTCAGATCAACTACTAATGCGCATCACTGCGAAT 240 QY 909 TTTAGCACTTGTCAACAATATATGCGTCAACGATCAACGAGCACAGAGCACATCATACTAATGCATTGCAT 300 QY 969 GGCTCTTGTGAAAAAAAAAAGGTTACTGAAAATGACATGCAATGCAT 300 QY 969 GGCTCTTGTGAAAAAAAAAAAAGGTTACTGGTAAATGACTGTGTGTTAGCA 1028

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SOURCE
ORGANISM
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JOURNAL
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TITLE
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AP005890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kikuchi, S., Satch, Y., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Shikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, B., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Riken, Kawai, T., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotami, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, T., Shiraki, T., Shiraki, T., Saito, R., Shiraki, T., Saito, R., Sasaki, T., Shiraki, T., Shiraki, T., Shiraki, T., Shiraki, T., Shiraki, T., Sasaki, T., Shiraki, T., Shiraki,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group) cDNA clone:J023078G01, full insert sequence.
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Science 301 (5631), 376-379 (2003)
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PLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, viridiplanteae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                            DB 6; Length 86; 3.5e-34;
                                                                                                                                                                                                                                                                                                                       0; Indels
'organism="synthetic construct"
                                                                                                                                                                                                                  4.9%; Scor.
100.0%; Pred. No. 5...
                                 /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="exon sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1747 INCCICCICTICTCCTTCAGIGCAAG 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 rrccrcrcrrcrrcrrcagracaag 86
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Best Local Similarity 100.(
Matches 86; Conservative
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REFERENCE
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AK100306
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KEYWORDS
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                                                                                                                                                                ORIGIN
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FAIRG Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIRG Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Kodama, T., Kurosaki, T., Kusumegi, T., Lul, M., Mana, J., Maran, T., Kurosaki, T., Kusumegi, T., Lul, M., Mana, J., Maran, Y., Maruno, K., Narikawa, R., Niikura, J., Oka, M., Kyu, R., Sugamo, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murzkami, K.
Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Haraoka, T., Hashawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Haraoka, T., Hashawa, T., Ida, J., Imamura, K., Imotani, K., Ishii, Y., Ilch, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Shinagawa, A., Shiraki, T., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Saco, K., Shibata, K., Shinagawa, A., Shiraki, T., Takahashi, F., Takahashi, F., Takahashi, F., Takahashi, F., Takahashi, S., Tanaka, T. Tomaru, A., Toya, T., Waki, K., Toya, T., Waki, K., Tona, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group) chromosome 9 clone B1029C06, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Rojima,K., Namiki,T.,
Chneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                       Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Submitted (27-AUG-2002) Spartment of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
1205-802, Japan (E-mail:8Kikuchi@mias.affrc.go.jp,
Tel:81-29-838-7007, Fas.81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
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HIG; HIGGS PHASEZ.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
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/mol_type="mRNA"
/cultivar="Nipponbare"
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
clone:B1029C06
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100.0%; Pred. No. 1.3e-17;
ive 0; Mismatches 0;
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/clone="J023078G01"
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Best Local Similarity
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Gaps

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Oryza sativa (japonica cultivar-group)

ENKaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ENKaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

SE lobases 1 to 135594)

SS Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L.L., Teltrin, T., Kan, M.M., Bera, J.J., Jin, S.S., Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.S., Riedmuller, S.B., Peterson, J.J., Quackenbush, J., Wang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.

Oryza sativa chromosome 3 BAC OSJNBb0097F01 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLN 12-MAR-2003
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genscan and Genscan+ (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-DEC-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 135594)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medical Center Dr. Rockville, MD 20850, USA 4 (bases 1 to 135594)
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Oryza sativa chromosome 3 BAC OSJNBb0097F01 genomic sequence,
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                                                                                         (japonica cultivar-group)"
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     the accession number will be preserved. Location/Qualifiers
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/organism=Oryza sativa ('organism=Oryza sativa ('cultivar="Nipponbare" | db xref="taxon:39947" | chromosome="9" | clone="OSJNBa0064123"
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NOTE: It currently consists of 1 contiggs Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NoTE: This is a "workfing draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and
                                                                                                                                Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Breath Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Breath Brogram; Kannondai 18-1-298-38-1441, Fazal 200-15p, URL: http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fazal 298-38-7468]

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is avvailable and the accession number will be preserved.
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AP005912.1 GI:25396710
HTG; HTGS PHASE2.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Evkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                    2 (bases 1 to 139653)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (13-NOV-2002) Takuji Sasaki, National Institute of
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
clone:OSJNBa0064123
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* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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100.0%; Pred. No. 3.3e-16;
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cultivar="Nipponbare"
/db_xref="taxon:39947"
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Published Only in Database (2002)
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FEATURES

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oin(15199. .15291,15955. .16184,16327. .16585,16680. .17351)
gene="OSJNBb0097P01.5"
codon_start=1
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AWRVPETLMLVSCEMBATRLIEVAHSNLQVRGTLFRRIHLGMPAAIAMNLFGDPAAEG
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TDKALEKVSEAASHAEAAKDAVDIABTLLSQPQPPLQLWAEWTSAAEKLVDQAALEAT
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SDAWTILLSRRRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /produci d="AAOGC329.1"

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RAVERARVRHSAREVRHSAREVGAATAIRVRRVGDGGARGGGGGEKKGLAWSRVVVLSGVGKLCAV

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DAGGEEVILHNDGQHRRVCRRRAWSTVSVSRFATLLPQRRAARRELRRGVAAVGFKFE
                                                                                                                                                                                                   FVNNILARRADDGTSTTVVEELEISFKLFNSRCMSGGSKRVVPSVDVAQVDAWIQYGM
QHVSKSFTLQLNYMLPINLHNSNSSNGCMQVLGSNKLMITCGGGATRLESMVLSINKA
CLRRLPTNVTLDSLVHLTLEDVDDLNQLLSTARCPSLRKLCLHKQTVSPATTTDQSLH
                                                                                                                                                                                                                                                                                                              ASIVQVEDMECVRIFETEMSSLRRPECNDHYNQTRIRLLRCCKFLQFLTLHLTTTQKD
GHDSABVELIKDIPQLPHATSLSLQVPAQVYDIASVLCLLTRCKFLKHLELNIKYCSM
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                                                                                                                                                                                                                                                                                         LESNELLKVSLDWIWSRALVLELRTPRLRVFHTRNASIGRLVISAPRLEELTFFYTRV
complement(join(6551. .6928,7019. .7198,7813. .8808))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted by fgenesh"
join(~15199. 15291,15955. 16184,16327. 16585,
16680. >17351)
/gene="OSJNBb0097F01.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10607. .12644
| gene="OSJNBb0097F01.4"
| dene="OSJNBb0097F01.4"
| join(1.10607. .10874,11173. .>12644)
| gene="OSJNBb0097F01.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(10607. .10874,11173. .12644)
/gene="OSJNBb0097F01.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="hypothetical protein"
                                                                                         product="hypothetical protein"
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(5199. .17351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5199. .17351
gene="OSJNBb0097F01.5"
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16421. 16448
/rpt_family="GC_rich"
16837. 16860
/rpt_family="GC_rich"
17838. 17904
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19289. .19415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="CT-rich"
19367. .19420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="tandem"
19801. .19835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .11347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15625. .15655
                                                                                                                                                                                                                                                                                                                                                                                                                                           ECRQIVHMD"
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        CDS
after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan.SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2511. .2542
/note="Region with dinucleotide (GA) repeat 16-17 copies"
7543. .2557
/note="VorInp OSJNBA0090L05 has 13 mononucleotide G
repeat in this region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="maaevwkaqegrluvebaairvdgyresihallpoltsssssmva
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daalllidhvgrledvogminaerlaavadleaaivavorsaemataarodvsgas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WFVRAQGGWRREDSARDRPAAAVKQSDGDEKGKRTDSEERMADGGAWLPAAARTAARR
GGRYERRULTGRSELINAGRGRVGTGERARSRWGRRGAAAASAALPLEGERKELRQGARY
PGREKAKGGGGKGALLLPFWEERDENEPRLTVLDARGMGRRAREDDAGDDCKKDGDGLK
ASADTVVVGASDDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'translation="MVAPGIKERREANGGAQPCARRRKGRHGAGAKEEAGGRSDGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6551..8808)
/gene="OSJNBD0097F01.3"
/note="predicted by fgenesh"
complement(join(<6551..6928,7019..7198,7813..>8808))
/gene="OSJNBD0097F01.3"
                                                                                                                                                                         http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2597. .2613
/note="Overlap OSJNBa0090L05 has 15 mononucleotide G repeat in this region."
/note..3062
/rpt_family="(TAGA)n"
4358. .4383
                                                                                                                                                                                                                                                                                   overlaps with rice BAC OSJNBa0013M12 (AC082644) and 00L05 (AC084765).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  1. .135594
/organism="Oryza gativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="predicted by fgenesh"
|oin(<1220. .1542,2036. .>2414)
|gene="OSJNBb0097F01.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="hypothetical protein"
protein_id="AA062320.1"
'db_xref="G1:28927674"
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gene="CSJNBb0097F01.2"

join (4384. .4586,4687. .4960)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="OSJNBb0097F01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(1220. .1542,2036. .2414)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="(CGAG)n"
4384. .4960
/gene="CSJNBb0097F01.2"
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1220. .2414
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="3"
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/rpt_family="tandem"
2511. ,2542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         map="near Y3870R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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OSJNBa0090L05
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.12084,
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/gene="OSJNAb0008A05.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDALUTRLAGALADWAAYNSTLRYAACWAASSDGFPGTTGYWHNIYGLUQCRPDLAP
PACRACLQALIVDMPQAFGGRIGGQFNAVWCNLRYETSVFYDGDPAVRLUASPSLEGP
NINGSTTLIIGNRRRRRPNAATVVSVLAAVITALLSYLSIYLWRKLQAKQCSPLAATA
QQLIVKQAASKQIKQGSTKSKQAMAYADGDGAALGEDVGEVGVDECAVAVVEGEA
VVAALSYARGFGDDVGTRSALVLRHLWVAPRKSSATASWSSTRAWRRPPRFRTAASPS
HRLGFBAAASPDRRHLTPADTADQDVEAGSLLFDLATLRKATANFAEVNKLGHGGFGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLLDSSMNPKISDFGLARLFDGNKTASVTSHVVGTLGYMAPEYAVLGLLSVKLDVYSF
QVLVLEVYTGRRNTDVFGAVEESNNLLSYWDHWVKGTPLAIVDASLLGDGRGPPESE
MIKCIQLGLLCVQENPADRPTMLHILVMLHDVDATSFAAPSKPAFTFVNGGHTTGSSS
NVAALSLNEVSISEFHPR"
16903. .16930
/note="Simple Sequence Repeat (ATAG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELTIGEOSMPOGGSLSVVRPOROFFENNAGNITRNOAPRATAGENTER CONTROLLED CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Putative polyprotein"
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KFLEGLNDELSYPLANTGDYHDFQXLVDKAIRQEDKYNRAEGKKRIAQFKTQGGNNQK
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WRQRRALEIKOYDMGTHYHPGKANNVADALSRKGYCNATEGRQLPLELCKEPERLNU
GIVSRGFYALLEAKPTLIDQVREAQINDPTOEIKGWRRGKAIGFLEDEGGTYWLGE
RSCVPDNKDLKOAILKRAHDTLYSIHPGSTRGYYQDLKERFFWAAARREFABYVNVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MTVPTMLWSTLVPLVLLAPLFSIPRHCRAQVLMNYSCNNGSSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENSTYDSNVRAVLATLSASTPNATTGFATASAGRGADTVWGLALCRGDTDHAVCASCV
AAVPALAFHQCRGVRDVTVFYDRCIARFSYGDFTARPDNTEVLMVSPSKYQATVNAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKGFLRDGEE1AVKRLDKASGOG1EOLRNELLLVAKLRHNNLAKLLGVC1KGEEKLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEYLPNRSLDTFLFDPEKRGQLIWETRYHIIHGTARGLVYLHEDSHIKIIHRDLKASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CQRVKAEHQKPAGLLQPLKI PEWKWEEIGMDFITGLPRTSSGHDSIWVIVDRLTKVAH
FIPVKTTYSGSRLAELYMARIVCLHGVPKKIVSDRGSQFTSNFWKKLQEEMGSKLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSPEEGDYVYIRVTPFRGVHRFHTKGKLAPRPVGPYKIVSRRGEVAYQLELPQSLAGV
HNVFHVSQLKKCLRVPTEEANLDQIEVQEDLTYVEKPIRILETNERRTRNRVIRFCKV
QWSNHSEEESTWEREDELKSAHPHLPASSSESRGRDSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAYHPQTDGQTERVNQ1LEDMLRACALDFGGSWDKNLPYAEFSYNNSYQASLQMAPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALYGRKCRIPLLWDQTGERQVFGTDILREAEEKVKIIQERLRVAQSRHKSYADNRRRD
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                                                                                                                                       7716. 7926,798 . 8122,9355 . 9443,9532 . 9772,11989 . 13110 . 1329,1335 . 14193) / gene="OSJNAD9008A65.2" / codon_start=1
                                                                                                                    note="Contains similarity to receptor-like protein
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/db_xref="GI:22655732"
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/note="Contains similarity to polyprotein"
complement (join(23976. .27756,27852. .28321))
/codon_start=1
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/note="Similar to truncator transposon"
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                                             complement (6525. .14193)
/gene="OSJNAb0008A05.2"
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Arizona, 303 Forbes, Tucson, AZ 85721, USA
The following sequence is an artificial clone that will be used for gap filling in the rice genome. There is 100 kb of sequence from the overlapping south clone (OSUNBAOOOBAOS) and 7982 bases of sequence from the overlapping south clone (OSUNBAOOOSAA4) and the gap filling sequence begins at 100,001 and ends at 116,384 for a total size of 124,366 bases. The gap filling sequence is 16,384 bases. The name (OSUNBAOOOBAOS) was derived from the location of the north clone and the 'A' stands for Artificial.
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LAQVARLGWVLQGCRAGGVQQGNQAQWEHFQHEVETTRTMRGELVDALKLTLQLLFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae;
1 (bases 1 to 124366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (21-AUG-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
3 (bases 1 to 124366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 124366)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Saski,C.,
Currie,J. and Collura,K.
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Saski, C. Currie, J. and Collura, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="Contains similarity to receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing, R.A., Yu, Y., Soderlund, C., Kim, H., Rambo, T., Saski, C., Currite, J., Collura, K. and Thurmond, S.K.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                   124366 bp DNA linear PLN 03-
Oryza sativa (japonica cultivar-group) chromosome 10 clone
OSJNAD0008A05, complete sequence.
AC131374
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/product="butative receptor-like protein kinase"
/protein_id="AAN04148.1"
/db_xref="GI:22655731"
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                                                                                                                                                  Length 135594;
                                                                                                                                                                                                                                                                                          7 GATAATAAAGTAAGTCACAAGAAAAATAAATAATAATTCCAAATTTTTTT
                                                                                                 2.8%; Score 50; DB 8; Lengtn 133.
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/sub_species="(japonica cultivar-group)"
/db_xref="taxon:39947"
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/note="Simple Sequence Repeat (TC)n"
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                                                                                                                                                                 100.0%; Pred. No.
/rpt_family="AT_rich"
complement(20634..21896)
/gene="OSJNBb0097F01.6"
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1994. .2011
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                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein"
/prodict="Hypothetical protein"
/protein id="AAN04122.1"
/protein id="AAN04122.1"
/protein id="MOPLVARPS"
/trainslation="WOPLVARPS"
SYTRRACRVPPLGAWRARPGRVVARHLPRGAALRDIPGPHPARGDDERMSPASNHNLA
QSVNWCCLRCASSGAWRTTWPSATSRGRCCATCTRSPTACTSSSTASTRRSSSPTALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTPPPSQTEISQDNLIPATWESINDEQWAEIGNNVQQLQEACLK
TFSIAQQGIVVQKTKFRTSCGEGGGSCTKDIKVEQDEEWQKVLTKFNQLAIQDHVDSA
VNHALINQSRVLVNTLANLIKSVVDGSIAEHEERGSVYLPGGEFPNYRELKTSIGGGR
FQDNVWYSKSKQPPTSGVFGSNTMIPEKLAEILKSVIPGSTQPSATEPIARRPFVIP
OPHTQQPSGQPIGSHTIRPQYCIQEPRTFSF"
43103. ,43154
                                                                                                                 SNSEDIPSVMPEAGGRNYIHAČQEVARIAIRELRDRYSDQLADTEYRYHPRQSQGSDR
SVETETGIRDATTRELLVERLIMADESRAETYLAAQDREDRRRGKICKLEDKVURLE
KELATLKGRAPPQKARIRLTRARRALFEVPRYQLAPKYRVVEKEVAPTLADPPVIIISD
DEEEESKRNHSKIEWVATQDDEDEPNEPSIDLRCSEELE"
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adilhsastygkilddkpvgqyidkaegylkdpssgsggaappppaagdaaabkpaaee
ppkepapaekeegkppsssegfglddvmkgaeslmekkgggeesagsggaagglfkma
                                                                   /translation="Myrcgglcyargivttpprapglewnipgleielysrdgcsewl
Glcnrmrrykpeylpgvegfigelrimspvigfgtappyaqiphdrheekcrvkvtln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tränslation="MDINMYTWGHCKLSRRSVQFKRIATLFTFLLFIIRQNLAPNAGL
HRLSISGEGDQTDWQNLLLDTERLRPLLLRHPKIMNLFRGHWEKMSSDANFNNTNIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Hypothetical protein"
complement(join(34658. .34708,35003. .35096,35507. .35520,
product="Putative gypsy-type retrotransposon protein"
protein id="AAN04151.1"
/db_xref="GI:22655734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(38823. .38999)
/note="Similar to Explorer_Os1 MITE-like element"
complement(40530. .41279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.7%; Score 48; DB 8; Length 124366; 100.0%; Pred. No. 4.9e-14; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                             complement (30001. 32200)
/note="Similar to truncator transposon"
complement (32582. 33127)
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protein_id="AAN04154.1"
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'protein id="AAN04153.1"
'db_xref="G1:22655736"
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complement(40530. .41279)
/gene="OSJNAD0008A05.7"
                                                                                                                                                                                                                                                                                                    /note="Hypothetical protein"
complement(32582. .33127)
/gene="OSJNAb0008A05.5"
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/gene="OSJNAb0008A05.6"
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gene="OSJNAb0008A05.8"
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                                                                                                                                                                                                                                                                            /gene="OSJNAb0008A05.5"
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/db_xref="G1:22655738"
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46561. .47056
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Best Local Similarity 100.(
Matches 48; Conservative
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Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://www.softberry.com/), http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHDM (Mark Borodovsky, http://genemark.biology.gatech.edu/GENSCAN.html), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits Genes without significant peptide similarity but with EST similarity, to other proteins protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tNNAs are predicted by tRNAscan-SE (Sean Eddy, Length Leng
                                                                                                                                                                                                                                                                                                                                                                                                                   AC091749 150465 bp DNA linear PLN 13-NOV-2001
Oryza sativa chromosome 10 BAC OSJNBb0008A05 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae, Oryza.

[ (bases 1 to 150465)

Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Moffat, K.S., Hill, J.N.,

Gansberger, K., Brenner, M., Burgess, S., Hance, M., Shvartabeyn, M.,

Tsitrin, T., Riggs, F., Helao, J., Zismann, V., Blunt, S., Pai, G.,

VanAken, S. E., Utterback, T.R., Feldblyum, T.V., Kalb, E.,

Quackenbush, J., Salzberg, S.L., White, O. and Fraser, C.M.

Oryza sativa chromosome 10 BAC OSJNBb0008A05 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-OCT-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA (bases 1 to 150465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC clone OSJNBb0008A05 is from Oryza sativa chromosome 10
The orientation of the sequence is from SP6 to T7 end of the BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-NOV-2001) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Oct 26, 2001 this sequence version replaced gi:15808580. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
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77
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / LTAINSTAIL OID "METTRINGSRDSNNASGSEEPINGARANGASDNSBSPPENPTIAQ VLDNGTOWNTWMOOMQRQYHQVLQQVQQQAQQQONPQFGPPPOSKLLEFLRVKPP TESTTVPI ETSTTVPI ETAHDWILAI EKKLNLLCQCONCOENCAPATHQLQGPASIWDNYWYTRPIG ABCTWPTEFRHSFNIKAQVPEGI VQQKKREFRSLQQGTYKTVI EYLHEFNRLARYABEDVR TDAEKQEKFMSGLDDGLTNQLI SRDYEDFEKLVDKAIRQEGCNKMNRKKRAAQFTTP
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2.7%; Score 48; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 4.7e-14;
Matches 48; Conservative 0; Mismatches 0;
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LEWPVDIVERGEGORGALDFEEDRYPERVOFTURDAY
LEWYLDFRTRARVTFTPDAPEBHVAAVTDAY PHREDRYFVAADAARDISADISADITAVQVR
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Identities 160 849 (of subject); contains pfam domain
DUF26 Domain of unknown function DUF26 e value 2 8e 22"
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join(<29419. .29431,29533. .30336,30684. .31133,31380. .31469,
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AAACRACLETIRVDMPKVFAGRIGGRFDAVWCHLRYETFLFYDGDPTVRLAASPSPGS
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GQGLEQLRNELLFVAKLRHNNLAKLLGVCIKGEEKLLIYEYLLPNRSLDTFLFDPEKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVGCKAKHTKLSVTLDLMKLKASNGWTDKSFTDLLGILKAMLPVENTLPETTYEAKQV
LCPLGLEVRRIHACPNDCILYHKQYADLDAYPVCKASRYKRKKSADEGNKSKRGGPRQ
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DIRXATANRPAEHNKIGHGGGGAVYKGFLPDVGEIAVKELDRTSGQGLEQLRVELLLVA
KLAHNNLAKLIGVCIKGDEKLLVYEFLPNRSLDTILFDPQKREQLSWETRYQIIHGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLLYLHEDSQIKITHEDLKASNVLLDSNWNPKISDFGLARLCSGTKTTSITSQVVGT
LGYMAPRYATGHLSVKVOVSFGILVLEIVYGRRNTDVPDABESSNILSYVRPIDQ
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ENPADRPTMLSVLVMLQDVDTTNFAAPSKPAFTFANVRNTTSSSPSAAALSANEVSIS
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OGYKTASITMIVVGTLGYMARBEYAVLGHVSVKLDVSFGGILVLBIVTSRUTDVSGEV
BESNNLLSYWDHWKGTPLEIADASLLGDGRSLSDMELLKCWHFGLLCVQENPUDRP
TMLDIILWMLHDVDTNSFVAPSKRAFTFAHGGNTTSSSQCVAALSTNEVSISEFVPR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative serine/threonine kinase"
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LAAVPAVAFGECRGDRDVAVFYDRCLARFSYADFTSRPDNTEVLIGSPSENRVTVDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEDEDELDMLIPSPLGDEMVDADHDLLQDMLCDVEDPAQNERDGMKFSRLVSDSGTPL
                                                                                                                                                                                                                                                                                                                                                   translation="MATRVLLSSKVILALVLASLFSLPRHGRALELMNWSCNNGSAYA"
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                                                                                                                                                                                                            /codon_start=1
product="putative serine/threonine kinase"
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                                                                                                                                                                    locus_tag="OSJNBa0093109.21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <29419. .>32693
   mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Dr. Rockville, MD 20850, USA
This is the pseudomolecule for rice chromosome 10, which was
constructed by resolving discrepancies between overlapping BACs,
trimming the overlap regions, and linking the unique sequences to
form a contigous sequence. Genes in individual BAC clone were
identified by a combination of several methods: Gene were
database and EST databases. Genes with similarity to other proteins
are named after the database hits. Genes without significant
peptide similarity but with EST similarity, that are
predicted by more than two gene prediction prodrams over most of
their length are annotated as hypothetical proteins. Genes
encoding ENNAs are predicted by tRNAscan-SE (Sean Eddy,
http://genome.wastl.edicted by tRNAscan-SE (Sean Eddy,
                                        Oryza sativa (japonica cultivar-group) chromosome 10, section 30 of AB017076 AE016959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <1. 90733
/hote="Chromosome Sequence Derivation: nucleotide sequence
in this region was derived from BAC clone OSJNBa0093109
(GB:AC090486)."
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RKPFSRRYVGALAVGFVQGRRQENSSSSGAPPPRFIPLPSYSSRFAGGGELDKVFD
SGLLSNSRLIASRKGLLVLELRRSSRAAVRLVVCNPWTGWATLPILAGKDRFGHYA
CALITEDDHEGAPDRLGFFWDAAFRLLVYKRRNFTACRSYMATLYTAMDAEGKLSGA
KIGGRRLGEWTGAYARGSVFWLLFVYRLGALKATTETFPSKWGSKLCFYGSP
VQNRQLAVTPDGRLCAVQVDRHVTSNNTVRINVISRHDGYGPPTWECDNARDVELNRV
                                PLN 06-JUN-2003
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e value 7 4e 47; contains pfam domain DUF26 Domain of
unknown function DUF26 e value 6 8e 19"
                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erhartoideae; Oryzaee; Oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Genomic Research, 9712
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Buell, C.R., Wing, R.A., McCombie, W.R., Messing, J. and Yuan, Q. Direct Submission

Direct Submission The Institute for Genomic Research, Submitted (05-MAY-2003) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Rice Chromosome 10 Sequencing Consortium
In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
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.538. .2977
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/locus_tag="OSJNBa0093109.21"
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                                                                                                                                                                               GI:31431167
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                                                                     DEFINITION
                                                                                                                                                                                                                                                                                 ORGANISM
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JOURNAL
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TITLE
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                                                                                                                                       ACCESSION
                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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AE017076
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DLYKPDPWOLPRMALYGEKEWYFFSPRDRKYPNGSRPNRAAGSGYWKATGADKPVGSP
KPVALKKALVFYAGKAPKGEKTNWIMHEYRLADVDRSARKKNSLRLDDWVLCRIYNKK
GGLEKPPAAAVAAAGMVSSGGGVQRKPMVGVNAAVSSPPEQKPVVAGPAFPDLAAYYD
                                                                                                                        Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G. Plant genes involved in defense against pathogens Patent: WO 030000898-A. 6089 03-JAN-2003; pathogens Participations AG (CH)
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Oryza sativa
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enhartoideae, Oryzea, Oryza,
I (bases 1 to 4817)
Yoon, U. H., Hahn, J. H. and Eun, M. - Y.
Molecular cloning of NAC6 gene in rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-APR-2000) Division of Cytogenetics, National Institute of Agricultural Science and Technology, Seodun-dong, Suweon 441-707, Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2000;
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3.5e-12;
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100.0%; Pred. No. 3...
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Direct Submission
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(of subject); contains pfam domain Cytidylyltrans Phosphatidate cytidylyltransferase e value 2 7e 41.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KES FDY PASHEDRLKNAAFKVNGNAMKNFKTKL VGETVINDANDDPREKFPWITTEQWW
ESTENAKKYTERSKASBAPKTNLLLGYKNOHPHALGTTGYTGAKEREBURDREBLEABESNTPL
VPGDI PHPRARNWARN GYKNDGTI FEMPNEBDGRYVKAI ELIVAEGQAS GRACS GRCE
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DDLLTKALGNKEHRGRTGGVGSS VPWKYGFPDYAWQYKKRTSNKARKOARLEAKIRES
ENPLET INSTENEKLESWRAKT IKREI IREBEGONPOAAATTHEBELGSPTGVRAKISCASTELA
ENPTSVDSA VDHITEPTSCTLTVRWPTFWRQECMENSGGOCAKVQVDS VKPEYELF
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MMNTYYATVMM"
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RPSDSMPRLHADSSCSEGVLSPEFACEVQSQPKISEWERTFATVGPINPAASILDPAG SGGLGGLGGGGSDPLLQDILMYWGKPF" 4581. .4586 /gene="NAC6" .; 0 Gaps 0; Query Match 2.5%; Score 45; DB 8; Length 4817; Best Local Similarity 100.0%; Pred. No. 3.1e-12; Matches 45; Conservative 0; Mismatches 0; Indels polyA_signal ORIGIN

Search completed: October 2, 2004, 13:18:15 Job time : 11071 secs

46 CAAAITITITAATAAGACGAGTGGTCAAACAGTACAAGTAAAAA 90

δ qq

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OGTAI20TC

nbxb0019P

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kt73b08.y nbxb0030K nbeb0047D

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OGOBG28TH

Oryza sat ZMMBBb018

Searched:

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kt71b05.y

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nbeb0047D
PUGDU05TD
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magualiophyta; Liliopsida; Poales; Poaceae;
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1 (bases I to 628)
Wing, R.A. and Dean, R.A.
Who R.A. and Dean, R.A.
Unpublished (1998)
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by DNA linear GSS 01

nbxb0072B19r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb0072B19r, genomic survey
AQ510840
AQ510840
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAMACAGCTATGACCATG
Class: BAC ends
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CG164014
AQ258985
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BI323424
BI450665
AQ287509
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Contact: Wing RA
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/lab_host="Leaf".
/lab_host="E. coli DH10B"
/clone lib="CuG1 Rice BAC Library"
/note="Vector: pBeloaAC1; Site 1: HindIII; Site 2:
/note="Vector: ppopulated areas to popular grains in the
world Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies: In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,664 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18, 432 clones (doubly spotted), represent
the whole library for colony screening."
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Oryza sativa (japonica cultivar-group)
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae; Oryzaae; Oryza,
1 (bases I to 748)
Ning, R.A. and Deah, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                                                          'organism="Oryza sativa (japonica cultivar-group)"
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100 Ordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwinged:emon.edu
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                                                                                                 mol type="genomic DNA"
strain="Japonica"
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High quality sequence stop: 416.
Location/Qualifiers
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ity sequence stop: 384
Location/Qualifiers
                                                                                                                                                      cultivar="Nipponbare"
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'clone="nbxb0072B19r"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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/mol_type="genomic DNA"
'organism="Oryza sativa (japonica cultivar-group)"
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Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: TAATACGACTCACTATAGGG
                                                   type="genomic DNA"
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Location/Qualifiers
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                                                                                                       'strain="Japonica"
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us-10-009-570-1.oligo.rst

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High quality sequence start: 59
High quality sequence stop: 437.
Location/Qualifiers
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1 (bases 1 to 537)
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                                                           Local Similarity
tes 30; Conserv
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AQ510840.1
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                                          Query Match
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HindIII; Rice is one of two most popular grains in the
world Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library contains 36.864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
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BR030004000 PLATE E02 13 017.abl OA Oryza sativa (japonica cultivar-group) cDNA Clone BR030004000 PLATE E02_13_017.abl similar to No protein aligment, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases I to 629)
1 (bases I to 629)
1 (bases II, Kawasaki, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Plunctional Genomics of Plant Stress Tolerance
Unpublished (2000)
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100.0%; Pred. No. 0.22;
tive 0; Mismatches 0; Indels
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Tel: 2172655473
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
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CA754682.1 GI:25798713
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                      Gaps
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Ming, R.A. and Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
Contact: Wing RA
                                                                                                                                                   0;
                                                                               1.7%; Score 30; DB 14; Length 629; 100.0%; Pred. No. 0.2; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
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Query Match Best Local S

Matches

RESULT 6 AQ510840/c LOCUS

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ACCESSION VERSION KEYWORDS TITLE JOURNAL COMMENT

AUTHORS REFERENCE

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (Baese it to 31)

1 (Raese it to 31)

2 (Raese it to 31)

2 Eark, S. H., Park, S. J., Chon, N. S., Je, B. I., Sun, B.,
Enk, S. H., Park, J. Y., Lee, E. J., Kim, M. J., Lee, J. J., Nam, M. H.,
Englid, large-scale generation of Ds transposant lines and analysis
of Ds loci in rice
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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nbxb0049E15r CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0049E15r, genomic survey
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Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 28; Conservative 0; Mismatches 0; Indels
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Contact: Chang-deok Han
Division of Applied Life Science, PMBBRC
Gyeongsang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 759 9363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdhan@nongae.gsnu.ac.kr
Location; chromosome 4 clone OSJNBb0034G17
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                                28 AAAAATAAATAATAATTCCAAATTTTTT
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzae; Diliopsida; Poales; Poaceae;
I. (bases 1 to 537)
Wing,R.A. and Dean,R.A.
Unpublished (1998)
                                                                 Gaps
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        DB 28; Length 537;
0.58;
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1.6%; Scor.
100.0%; Pred. No. c..
'.. 0; Mismatches
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High quality sequence stop: 437.
Location/Qualifiers
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                                                                 29; Conservative
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//lab_host="leaf"
//la
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
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A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
Clemson University
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        Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 31
High quality sequence stop: 404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Nipponare"
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/clone="nbx0049815r"
/tissue_type="Leaf"
/tissue_type="Leaf"
/tissue_type="Leaf"
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/clone lib="CuGI Rice BAC Library"
/note="Vector: pBeloBACI1; Site_1: HindIII; Site 2:
/indaili; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics. rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional clothing, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128 kWh varviding 128 kWh varviding 128 kMb varv
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Epermatophyta; Mamonliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzeae; Oryza.

1 (bases 1 to 452)
Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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'organism="Oryza sativa (japonica cultivar-group)"
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                                                         100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
                                                                                                                                                                                                                                                 Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Japonica"
                                                                                                                                                                                                         Email: rwing@clemson.edu
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Best Local Similarity 100.0
Matches 28; Conservative
                                           Clemson University
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Gaps

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GSS 03-NOV-1999

DEFINITION

LOCUS

RESULT 9 AQ860090

ACCESSION

VERSION KEYWORDS

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

ORGANISM

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/organism="Oryza sativa"
                     class: BAC ends
High quality sequence stop: 286.
Location/Qualifiers
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  Seq primer: GGAAACAGCTATGACCATG
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                                                                                                                                                                                                                  'cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                        /tissue_type="Leaf"
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/lab host="Leaf"
/lab host="Eaf"
/lab host="Eaf"
/lab host="Eaf"
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/note="Vector: pBacCladigo; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBacCladigo; Site_1: EcoRI; Rice is the most important food_crop in the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocoryledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 411 Mpp (Arumganathan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Gryza sativa, Nipponbare variety using EcoRI as the cloning ensyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Curyza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 623)
Wing,R.A. and Dean,R.A.
Whophished (1998)
Contact: Wing RA
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|mol_type="genomic DNA"
|strain="Japonica"
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Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 28
High quality sequence stop: 438.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 AAAATAAATAATTACCAAATTTTTT 237
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                                                                                                                                                                                                                                                                 /cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ258100
AQ258100.1 GI:3782582
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AQ258100/c
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/tissue type="Loaf" | 
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I (bases I to 65.2)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.E., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

A Gene Expression Screen in Oryza sativa
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Organism="Oryza sativa (japonica cultivar-group)"
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|strain="Japonica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3mail: webmaster@estarray.org, URL: http://www.estarray.org
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100.0%; Pred. No. 1.3;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tal: 0086-571-86892051
Fax: 0086-571-86961525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
Contact: Haitao Dong, Debao Li
Bioinfomatics and Gene Network Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 ATTTTTTAATAAGACGAGTGGTCAAAC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 ATTTTTTAATAAGACGAGTGGTCAAAC 76
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OGTATAOTH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0389C15, CC692659
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                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Bermatophyta; Bagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 783)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, M., Raser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other_GSSS: OGTAL20TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 70;
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Click, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Conscrium for Maize Genomics
Unpublished (2002)
Other GSSS: OGTAL20TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 AATTITITAATAAGACGAGTGGTCAAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 783
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
                                                                                                                          CC692659.1 GI:32097435 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC692657.1 GI:32097433
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                                                                                                                                                                           Zea mays
Zea mays
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              CC692659
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
E 1 (bases 1 to 694)
S Wing, Yu, Yi, Kim, H.R., Collura, K., Pries, G., Currie, J.,
Soderlund, C. and Hatfield, J.
Sequencing of Sorghum BAC ends.
http://genome.arizona.edu/stc/sorghum
L Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP_Ba0019009.f SP_Ba Sorghum propinguum genomic clone SP_Ba0019009 5', genomic survey sequence.
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O
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M.grisea"
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                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
TTE: 520 626 3967
Fax: 520 621 9288
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                                                                                                                                                                                                                                            DB 12; Length 652; 1.3;
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100.0%; Pred. No. 1.2;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                  542 AATAAGACGAGTGGTCAAACAGTACAAG 569
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Plate: 0019 row: 0 column: 09
Seg primer: atc agc ggc cgc gat cc
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://genome.arizona.edu
PCR PRimers
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Best Local Similarity 100.0
Matches 28; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL COMMENT

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Search completed: October 2, 2004, 15:13:13 Job time: 6892 secs